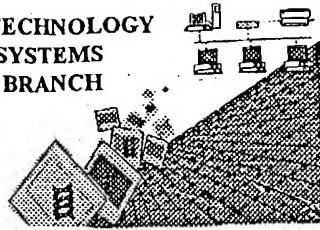# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/817,530

Source: 1FWO

Date Processed by STIC: 10/5/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
>   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
<u>Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:</u>

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/817,530

DATE: 10/05/2004
TIME: 10:34:02

Input Set : A:\Sequence.List.for.10817530.txt
Output Set: N:\CRF4\10052004\J817530.raw

```
 3 <110> APPLICANT: Braun, Werner
 4         Mathura, Venkatarajan S.
 5         Schein, Catherine H.
 7 <120> TITLE OF INVENTION: PHYSICAL-CHEMICAL PROPERTY BASED SEQUENCE MOTIFS AND METHODS
 8         REGARDING SAME
10 <130> FILE REFERENCE: 265.00400101
12 <140> CURRENT APPLICATION NUMBER: 10/817,530
13 <141> CURRENT FILING DATE: 2004-04-02
15 <150> PRIOR APPLICATION NUMBER: US 60/460,769
16 <151> PRIOR FILING DATE: 2003-04-04
18 <160> NUMBER OF SEQ ID NOS: 5
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 10
24 <212> TYPE: PRT
```
C--> 25 <213> ORGANISM: ARTIFICIAL MEMBER OF DNase-I SUPERFAMILY
W--> 27 <220> FEATURE:
W--> 27 <223> OTHER INFORMATION:
W--> 27 <400> 1
```
29 Pro Asp Ile Leu Cys Leu Gln Glu Thr Lys
30 1               5                   10
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 275
35 <212> TYPE: PRT
```
C--> 36 <213> ORGANISM: ARTIFICIAL MEMBER OF DNase-I SUPERFAMILY
W--> 38 <220> FEATURE:
W--> 38 <223> OTHER INFORMATION:
W--> 38 <400> 2
```
40 Leu Tyr Glu Asp Pro Pro Asp Gln Lys Thr Ser Pro Ser Gly Lys Pro
41 1               5                   10                  15
44 Ala Thr Leu Lys Ile Cys Ser Trp Asn Val Asp Gly Leu Arg Ala Trp
45              20                  25                  30
48 Ile Lys Lys Lys Gly Leu Asp Trp Val Lys Glu Glu Ala Pro Asp Ile
49              35                  40                  45
52 Leu Cys Leu Gln Glu Thr Lys Cys Ser Glu Asn Lys Leu Pro Ala Glu
53         50                  55                  60
56 Leu Gln Glu Leu Pro Gly Leu Ser His Gln Tyr Trp Ser Ala Pro Ser
57 65                  70                  75                  80
60 Asp Lys Glu Gly Tyr Ser Gly Val Gly Leu Leu Ser Arg Gln Cys Pro
61              85                  90                  95
64 Leu Lys Val Ser Tyr Gly Ile Gly Asp Glu Glu His Asp Gln Glu Gly
65              100                 105                 110
68 Arg Val Ile Val Ala Glu Phe Asp Ser Phe Val Leu Val Thr Ala Tyr
```

[Handwritten annotations on the right side of the page:]

pp 1-4, 6

Does Not Comply
Corrected Diskette Needed

delete; give source of genetic material

(circled) ARTIFICIAL MEMBER OF DNase-I SUPERFAMILY

Move down to <223> line.

Per 1.823 f Sequence Rules, the explanation for Artificial Sequence goes on <223> line. Please insert a <220> above <223>. Do not insert response to <220> — it is a header only.

```
                 RAW SEQUENCE LISTING          DATE: 10/05/2004
                 PATENT APPLICATION:  US/10/817,530     TIME: 10:34:02

                 Input Set : A:\Sequence.List.for.10817530.txt
                 Output Set: N:\CRF4\10052004\J817530.raw

69          115                120                125
72 Val Pro Asn Ala Gly Arg Gly Leu Val Arg Leu Glu Tyr Arg Gln Arg
73     130                135                140
76 Trp Asp Glu Ala Phe Arg Lys Phe Leu Lys Gly Leu Ala Ser Arg Lys
77 145                150                155               160
80 Pro Leu Val Leu Cys Gly Asp Leu Asn Val Ala His Glu Glu Ile Asp
81             165                170                175
84 Leu Arg Asn Pro Lys Gly Asn Lys Lys Asn Ala Gly Phe Thr Pro Gln
85         180                185                190
88 Glu Arg Gln Gly Phe Gly Glu Leu Leu Gln Ala Val Pro Leu Ala Asp
89         195                200                205
92 Ser Phe Arg His Leu Tyr Pro Asn Thr Pro Tyr Ala Tyr Thr Phe Trp
93     210                215                220
96 Thr Tyr Met Met Asn Ala Arg Ser Lys Asn Val Gly Trp Arg Leu Asp
97 225                230                235               240
100 Tyr Phe Leu Leu Ser His Ser Leu Leu Pro Ala Leu Cys Asp Ser Lys
101             245                250                255
104 Ile Arg Ser Lys Ala Leu Gly Ser Asp His Cys Pro Ile Thr Leu Tyr
105         260                265                270
108 Leu Ala Leu
109         275
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 268
114 <212> TYPE: PRT
```
C--> 115 <213> ORGANISM: ARTIFICIAL MEMBER OF DNase-I SUPERFAMILY
W--> 117 <220> FEATURE:
W--> 117 <223> OTHER INFORMATION:
W--> 117 <400> 3
```
119 Met Lys Phe Val Ser Phe Asn Ile Asn Gly Leu Arg Ala Arg Pro His
120 1              5                10                15
123 Gln Leu Glu Ala Ile Val Glu Lys His Gln Pro Asp Val Ile Gly Leu
124         20                25                30
127 Gln Glu Thr Lys Val His Asp Asp Met Phe Pro Leu Glu Glu Val Ala
128         35                40                45
131 Lys Leu Gly Tyr Asn Val Phe Tyr His Gly Gln Lys Gly His Tyr Gly
132     50                55                60
135 Val Ala Leu Leu Thr Lys Glu Thr Pro Ile Ala Val Arg Arg Gly Phe
136 65                70                75                80
139 Pro Gly Asp Asp Glu Glu Ala Gln Arg Arg Ile Ile Met Ala Glu Ile
140         85                90                95
143 Pro Ser Leu Leu Gly Asn Val Thr Val Ile Asn Gly Tyr Phe Pro Gln
144         100                105                110
147 Gly Glu Ser Arg Asp His Pro Ile Lys Phe Pro Ala Lys Ala Gln Phe
148     115                120                125
151 Tyr Gln Asn Leu Gln Asn Tyr Leu Glu Thr Glu Leu Lys Arg Asp Asn
152     130                135                140
155 Pro Val Leu Ile Met Gly Asp Met Asn Ile Ser Pro Thr Asp Leu Asp
156 145                150                155               160
159 Ile Gly Ile Gly Glu Glu Asn Arg Lys Arg Trp Leu Arg Thr Gly Lys
```

RAW SEQUENCE LISTING   DATE: 10/05/2004
PATENT APPLICATION: US/10/817,530   TIME: 10:34:02

Input Set : A:\Sequence.List.for.10817530.txt
Output Set: N:\CRF4\10052004\J817530.raw

```
160                   165              170              175
163 Cys Ser Phe Leu Pro Glu Glu Arg Glu Trp Met Asp Arg Leu Met Ser
164                   180              185              190
167 Trp Gly Leu Val Asp Thr Phe Arg His Ala Asn Pro Gln Thr Ala Asp
168          195              200              205
171 Arg Phe Ser Trp Phe Asp Tyr Arg Ser Lys Gly Phe Asp Asp Asn Arg
172      210              215              220
175 Gly Leu Arg Ile Asp Leu Leu Leu Ala Ser Gln Pro Leu Ala Glu Cys
176 225              230              235              240
179 Cys Val Glu Thr Gly Ile Asp Tyr Glu Ile Arg Ser Met Glu Lys Pro
180              245              250              255
183 Ser Asp His Ala Pro Val Trp Ala Thr Phe Arg Arg
184              260              265
187 <210> SEQ ID NO: 4
188 <211> LENGTH: 258
189 <212> TYPE: PRT
-> 190 <213> ORGANISM: ARTIFICIAL MEMBER OF DNase-I SUPERFAMILY
-> 192 <220> FEATURE:
-> 192 <223> OTHER INFORMATION:
-> 192 <400> 4
194 Leu Lys Ile Ala Ala Phe Asn Ile Arg Thr Phe Gly Glu Thr Lys Met
195 1                 5                10               15
198 Ser Asn Ala Thr Leu Ala Ser Tyr Ile Val Arg Ile Val Arg Arg Tyr
199              20               25               30
202 Asp Ile Val Leu Ile Gln Glu Val Arg Asp Ser His Leu Val Ala Val
203          35               40               45
206 Gly Lys Leu Leu Asp Tyr Leu Asn Gln Asp Asp Pro Asn Thr Tyr His
207      50               55               60
210 Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr
211 65               70               75               80
214 Leu Phe Leu Phe Arg Pro Asn Lys Val Ser Val Leu Asp Thr Tyr Gln
215              85               90               95
218 Tyr Asp Asp Gly Cys Cys Gly Asn Asp Ser Phe Ser Arg Glu Pro Ala
219          100              105              110
222 Val Val Lys Phe Ser Ser His Ser Thr Lys Val Lys Glu Phe Ala Ile
223      115              120              125
226 Val Ala Leu His Ser Ala Pro Ser Asp Ala Val Ala Glu Ile Asn Ser
227      130              135              140
230 Leu Tyr Asp Val Tyr Leu Asp Val Gln Gln Lys Trp His Leu Asn Asp
231 145              150              155              160
234 Val Met Leu Met Gly Asp Phe Asn Ala Asp Cys Ser Tyr Val Thr Ser
235              165              170              175
238 Ser Gln Trp Ser Ser Ile Arg Leu Arg Thr Ser Ser Thr Phe Gln Trp
239              180              185              190
242 Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Ser Thr Asn Cys Ala
243          195              200              205
246 Tyr Asp Arg Ile Val Val Ala Gly Ser Leu Leu Gln Ser Ser Val Val
247      210              215              220
250 Pro Gly Ser Ala Ala Pro Phe Asp Phe Gln Ala Ala Tyr Gly Leu Ser
```

```
251 225                   230                 235                  240
254 Asn Glu Met Ala Leu Ala Ile Ser Asp His Tyr Pro Val Glu Val Thr
255                  245                250                255
258 Leu Thr
262 <210> SEQ ID NO: 5
263 <211> LENGTH: 336
264 <212> TYPE: PRT
C--> 265 <213> ORGANISM: ARTIFICIAL MEMBER OF DNase-I SUPERFAMILY
W--> 267 <220> FEATURE:
W--> 267 <223> OTHER INFORMATION:
W--> 267 <400> 5
269 Tyr Asp Pro Ile His Glu Tyr Val Asn His Glu Leu Arg Lys Arg Glu
270 1              5                 10              15
273 Asn Glu Phe Ser Glu His Lys Asn Val Lys Ile Phe Val Ala Ser Tyr
274             20                25                30
277 Asn Leu Asn Gly Cys Ser Ala Thr Thr Lys Leu Glu Asn Trp Leu Phe
278             35           .    40                45
281 Pro Glu Asn Thr Pro Leu Ala Asp Ile Tyr Val Val Gly Phe Gln Glu
282    50                 55               60
285 Ile Val Gln Leu Thr Ser Ala Asp Pro Ala Lys Arg Arg Glu Trp Glu
286 65                 70               75               80
289 Ser Cys Val Lys Arg Leu Leu Asn Gly Lys Cys Thr Ser Gly Pro Gly
290             85                90                95
293 Tyr Val Gln Leu Arg Ser Gly Gln Leu Val Gly Thr Ala Leu Met Ile
294             100               105               110        .
297 Phe Cys Lys Glu Ser Cys Leu Pro Ser Ile Lys Asn Val Glu Gly Thr
298         115               120               125
301 Val Lys Lys Thr Gly Leu Gly Asn Lys Gly Ala Val Ala Ile Arg Phe
302     130               135               140
305 Asp Tyr Glu Asp Thr Gly Leu Cys Phe Ile Thr Ser His Leu Ala Ala
306 145               150               155               160
309 Gly Tyr Thr Asn Tyr Asp Glu Arg Asp His Asp Tyr Arg Thr Ile Ala
310             165               170               175
313 Ser Gly Leu Arg Phe Arg Arg Gly Arg Ser Ile Phe Asn His Asp Tyr
314             180               185               190
317 Val Val Trp Phe Gly Asp Phe Asn Tyr Arg Ile Ser Leu Thr Tyr Glu
318         195               200               205
321 Glu Val Val Pro Cys Ile Ala Gln Gly Lys Leu Ser Tyr Leu Phe Glu
322     210               215               220
325 Tyr Asp Gln Leu Asn Lys Gln Met Leu Thr Gly Lys Val Phe Pro Phe
326 225               230               235               240
329 Phe Ser Glu Leu Pro Ile Thr Phe Pro Pro Thr Tyr Lys Phe Asp Ile
330             245               250               255
333 Gly Thr Asp Ile Tyr Asp Thr Ser Asp Lys His Arg Val Pro Ala Trp
334             260               265               270
337 Thr Asp Arg Ile Leu Tyr Arg Gly Glu Leu Val Pro His Ser Tyr Gln
338             275               280               285
341 Ser Val Pro Leu Tyr Tyr Ser Asp His Arg Pro Ile Tyr Ala Thr Tyr
342     290               295               300
```

RAW SEQUENCE LISTING   DATE: 10/05/2004
PATENT APPLICATION: **US/10/817,530**   TIME: 10:34:02

Input Set : **A:\Sequence.List.for.10817530.txt**
Output Set: **N:\CRF4\10052004\J817530.raw**

```
345 Glu Ala Asn Ile Val Lys Val Asp Arg Glu Lys Lys Ile Leu Phe
346 305             310             315             320
349 Glu Glu Leu Tyr Asn Gln Arg Lys Gln Glu Val Arg Asp Ala Ser Gln
350             325             330             335
```

erro Explaration

Input Set : A:\Sequence.List.for.10817530.txt
Output Set: N:\CRF4\10052004\J817530.raw

Use of <220> Feature(NEW RULES):
Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:1,2,3,4,5

VERIFICATION SUMMARY   DATE: 10/05/2004
PATENT APPLICATION: **US/10/817,530**   TIME: 10:34:03

    Input Set : **A:\Sequence.List.for.10817530.txt**
    Output Set: **N:\CRF4\10052004\J817530.raw**

```
L:25 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:27 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:27 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:27 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27
L:36 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:38 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:38 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:38 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:38
L:115 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:117 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:117 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:117 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:117
L:190 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:192 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:192 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:192 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:192
L:265 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:267 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:267 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:267 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:267
```